

1 CCTCTGTCCTTCCCCCAGGTCCCTTTTTCCTTCTCTCTCTCTCTTTATTTCTCTTT 60
 61 TCATAAGCATATTTCTTCTCTCTCTAGGGTTTTCACTTTCACCTGAAATAGTGTGTTAA 120
 121 ATTGAATGATATGTTAGGATCCTTTGGTTCTTCATCATCTCAATCTCACCCATCATGA 180
 M L G S F G S S S S Q S H P H H D
 181 TGAAGAATCTTCTGATCATCATCAACACGCTAGATTACCGCTACTGCTACAACATATCAC 240
 E E S S D H H Q Q R R F T A T A T T I T
 241 CACCACCACCATCACTACCTACCAGCTATTCAAATCCGCCAGCTACTCATTAGCTGTGC 300
 T T T I T T S P A I Q I R Q L L I S C A
 301 GGAGTTGATTTTCGAGTCCGATTCTCGGCCGCGAAAAGACTCCTTACTATATATCAAC 360
 E L I S Q S D F S A A K R L L T I L S T
 361 TAACTCATCTCCTTTTGGTGATTCAACTGAACGGTTAGTCCATCAATTACTCGGCACT 420
 N S S P F G D S T E R L V H Q F T R A L
 421 TTCCCTTCGCTCAACCGCTATATATCGTCAACCACCAATCATTTTCATGACACCTGTGA 480
 S L R L N R Y I S S T T N H F M T P V E
 481 AACAACTCCAAGTCTTCTTCTTCTTCGTCATCATTAGCTCTAATTCAATCATCATATCT 540
 T T P T D S S S S S S L A L I Q S S Y L
 541 ATCTCTAAACCAAGTTACCCCTTTTCATAAGGTTTACTCAATTAACCGCTAATCAAGCGAT 600
 S L N Q V T P F I R F T Q L T A N Q A I
 601 TTTAGAAGCGATTAAACGGTAATCATCAAGCAATCCACATCGTTGATTTTCGACATTATCA 660
 L E A I N G N H Q A I H I V D F D I N H
 661 CGGGGTTCAATGGCCACCGTTAATGCAAGCACTAGCTGATCGTTACCGTCTCCACTCT 720
 G V Q W P P L M Q A L A D R Y P A P T L
 721 TCGAATCACCGGTACTGGAATGACCTTGATACCCCTTCGTAGAACAGGTGATCGTTTAGC 780
 R I T G T G N D L D T L R R T G D R L A
 781 TAAATTTGCTCACTCATTAGGGTTGAGATTTCAATTCCATCCTCTTTATATAGCCAATAA 840
 K F A H S L G L R F Q F H P L Y I A N N
 841 TAACCACGATCAGATGAAGATCCTTCTATTATTTCTCCATTGTACTACTCCCTGATGA 900
 N H D H D E D P S I I S S I V L L P D E
 901 AACCTAGCTATCAACTGTGTTTTCTACCTCCACCGCCTTTTAAAGACCGCGAAAAGTT 960
 T L A I N C V F Y L H R L L K D R E K L
 961 AAGGATTTTTTTGCGATAGGGTTAAGTCAATGAACCCATAAATTGTTACAATCGCGAGAA 1020
 R I F L H R V K S M N P K I V T I A E K
 1021 GGAAGCAAATCATAACCATCCTCTTTTTTTTCAAAAGATTTCATCGAGGCGTTGGATTATTA 1080

Fig. [5 contd.] 5A

E A N H N H P L F L Q R F I E A L D Y Y
 1081 TACAGCTGTGTTGATTCACTGGAAGCTACATTGCCACCGGTTAGTCGAGAGAGGATGAC 1140
 T A V F D S L E A T L P P G S R E R M T
 1141 AGTTGAACAAGTGTGGTTTGGGAGAGAGATTGTTGATATCGTTGCGATGGAAGGAGATAA 1200
 V E Q V W F G R E I V D I V A M E G D K
 1201 AAGGAAAGAAAGACATGAAAGGTTTAGATCATGGGAAGTTATGTTGAGGAGTTGTGGATT 1260
 R K E R H E R F R S W E V M L R S C G F
 1261 TAGTAATGTTGCTTTAAGCCCTTTTCATTATCACAAGCTAAGCTTCTTTTGAGACTTCA 1320
 S N V A L S P F A L S Q A K L L L R L H
 1321 TTATCCTTCTGAAGGCTATCAACTCGGAGTTTCGAGTAATCTTTCTTCTTAGGTTGGCA 1380
 Y P S E G Y Q L G V S S N S F F L G W Q
 1381 AAATCAACCCCTTTTCTCCATCTCGTCTTGGCGTTGAGAAAACTATCAAATAGCCAACT 1440
 N Q P L F S I S S W R (SEQ ID NO: 2)
 1441 TCAGAGGGTAATTAAAGACTACTGATAGTTTAGGAGGGATCTGAAGAAAACGCGTGGAGTG 1500
 1501 AAAACCCTAATAACCAGATTTTCTAATGAAGTTGTAGTAGTAGAAAATTTGCATGGTGAA 1560
 1561 GAACAATATTGAAGAGGTATTGAAATTTTCATGTTTTTTTTGTTTTACTTATTGATATGAA 1620
 1621 TGTTTTAAATTTTTTAACATAGAGGACTAGGTTGATGATATATAGTATTTAAGTTAACTA 1680
 1681 GTCTTTGTATAACGCAAGATCTTGATCAACTTATTTTTATTTTAATTA 1729 (SEQ ID NO: 1)

Fig. 5 B

1	ATGTTAGGATCCTTTGGTTCTTCATCATCTCAATCTCACCTCATCATGATGAAGAATCT	60
1	M L G S F G S S S S Q S H P H H D E E S	20
61	TCTGATCATCATCAACGGCGTAGATTCACCGCTACTACTACAATATCACCACCACCACC	120
21	S D H H Q R R R F T A T T T T I T T T T	40
121	ACAACGACCTCACCAGCTATTCAAATCCGCCAGCTACTCATTAGCTGTGCGGAGTTGATT	180
41	T T T S P A I Q I R Q L L I S C A E L I	60
181	TCGCGGTCCGATTTCTCGGCCGCGAAAAGACTCCTTACCATATTATCAACTAACTCTTCT	240
61	S R S D F S A A K R L L T I L S T N S S	80
241	CCTTTTGGTGATTCAACTGAACGGTTAGTCCATCAGTTTACTCGCGCACTTTCCCTTCGT	300
81	P F G D S T E R L V H Q F T R A L S L R	100
301	CTCAACCGCTATATATCGTCAACCACCAATCATTTTCATGACACCTGTTGAAACAATCCA	360
101	L N R Y I S S T T N H F M T P V E T T P	120
361	ACTGATTCTTCATCTTCGTTGCCATCGTCATCATTAGCTCTAATTCAATCATCATATCAT	420
121	T D S S S S L P S S S L A L I Q S S Y H	140
421	TCTCTAAATCAAGTTACCCCTTTTATAAGGTTTACTCAATTAACCGCTAATCAAGCGATT	480
141	S L N Q V T P F I R F T Q L T A N Q A I	160
481	TTAGAAGCGATTAAACGGTAATCATCAAGCAATCCACATCGTTGATTTCGACATTAATCAC	540
161	L E A I N G N H Q A I H I V D F D I N H	180
541	GGGGTTCAATGGCCACCGTTAATGCAAGCACTAGCTGATCGTTACCCTGCTCCTACTCTT	600
181	G V Q W P P L M Q A L A D R Y P A P T L	200
601	CGAATCACCGGTACTGGAAATGACCTTGATACCCTTCGTAGAACAGGTGATCGTTTAGCT	660
201	R I T G T G N D L D T L R R T G D R L A	220
661	AAATTTGCTCACTCATTAGGGTTGAGATTTCAATTCATCCTCTTTATATCGCCAATAAT	720
221	K F A H S L G L R F Q F H P L Y I A N N	240
721	AACCGCGATCACGGTGAAGATCCTTCTATTATTTCTCCATTGTACTTCTCCCTGATGAA	780
241	N R D H G E D P S I I S S I V L L P D E	260
781	ACCCTAGCTATCAACTGTGTTTTCTATCTCCACCGCCTTTTAAAAGACCGCGAAAAATTA	840
261	T L A I N C V F Y L H R L L K D R E K L	280

Fig.[6 contd.] 6A

841 AGGATTTTTTGCATAGGGTTAAGTCAATGAACCCTAAAATTGTTACAATCGCGGAGAAG 900
 281 R I F L H R V K S M N P K I V T I A E K 300
 901 GAAGCAAATCATAACCATCCTCTTTTTTACAAAGATTTATCGAGGCGTTGGATTATTAT 960
 301 E A N H N H P L F L Q R F I E A L D Y Y 320
 961 ACAGCTGTGTTTGATTCAATTGGAAGCTACATTGCCACCGGTTAGTCGTGAGAGGATGACA 1020
 321 T A V F D S L E A T L P P G S R E R M T 340
 1021 GTTGAACAAGTGTGGTTTGGGAGAGAAATTGTTGATATCGTGGCGATGGAAGGAGATAAA 1080
 341 V E Q V W F G R E I V D I V A M E G D K 360
 1081 AGGAAAGAAAGACATGAAAGGTTTAGATCATGGGAAGTTATGTTGAGGAGTTGTGGATTT 1140
 361 R K E R H E R F R S W E V M L R S C G F 380
 1141 AGTAATGTTGCTTTAAGCCCTTTTGCATTATCACAAGCTAAGCTTCTTTTGAGACTACAT 1200
 381 S N V A L S P F A L S Q A K L L L R L H 400
 1201 TATCCTTCTGAAGGCTATCAACTCGGAGTTTCGAGTAATTCTTTCTTCTTAGGTTGGCAA 1260
 401 Y P S E G Y Q L G V S S N S F F L G W Q 420
 1261 AATCAACCTCTTTTCTCCATCTCGTCTTGGCGTTGA 1296 (SEQ ID NO: 9)
 421 N Q P L P S I S S W R * 432 (SEQ ID NO: 10)

Fig. 6B

1 GAGAGGTCATCAAACCCTAGCAGTCCACCTCCATCTCTCCGCATAACCGGATGCGGTCGA 60
 E R S S N P S S P P P S L R I T G C G R
 61 GATGTAACCGGATTAAACCGAACTGGAGACCGGTTAACCCGGTTCGCTGACTCTTTAGGT 120
 D V T G L N R T G D R L T R F A D S L G
 121 CTCCAATTCAGTTTCACACGCTAGTGATCGTAGAAGAAGATCTCGCCGGACTTTTGCTA 180
 L Q F Q F H T L V I V E E D L A G L L L
 181 CAGATCCGATTGTTAGCTCTCTCAGCCGTACAAGGAGAGACCATTGCCGTCAATTGTGTT 240
 Q I R L L A L S A V Q G E T I A V N C V
 241 CACTTCCTCCACAAAATATTTAACGACGATGGAGATATGATCGGTCACTTCTTGTCAGCG 300
 H F L H K I F N D D G D M I G H F L S A
 301 ATCAAGAGCTTAAACTCTAGAACTCGTTACAATGGCAGAGAGAGAAGCTAATCATGGAGAT 360
 I K S L N S R I V T M A E R E A N H G D
 361 CACTCGTTCTTGAATAGATTCTCTGAGGCAGTGGATCATTACATGGCGATCTTTGATTGG 420
 H S F L N R F S E A V D H Y M A I F D S
 421 TTGGAAGCGACGTTGCCGCCAAATAGCCGAGAGAGACTAACCTAGAGCAACGGTGGTTC 480
 L E A T L P P N S R E R L T L E Q R W F
 481 GGTAAGGAGATTTTGGATGTTGTGGCGGCGAAGAGACGGAGAGAAAGCAAAGACATCGG 540
 G K E I L D V V A A E E T E R K Q R H R
 541 AGGTTTGAGATTTGGGAAGAGATGATGAAGAGGTTTGGTTTCGTTAACGTTCTTATTGGA 600
 R F E I W E E M M K R F G F V N V P I G
 601 AGCTTTGCTTTGTCTCAAGCTAAGCTTCTTCTTAGACTTCATTATCCTTCAGAAGGTTAT 660
 S F A L S Q A K L L L R L H Y P S E G Y
 661 AATCTTCAGTTCCTTAACAATTCTTTG 687 (SER 1A NO:13)
 N L Q F L N N S L (SER 1A NO:14)

Fig. 7

LsAt	1	MLGSFGSSSSQSHPHHDEESSDDHHQ	RRFTAT	TTTTTT	TTSPAIQIRQLLISCAELI
LsLe	1	MLGSFGSSSSQSHPHHDEESSDDHHQ	RRFTAT	TTTTTT	TTSPAIQIRQLLISCAELI
LsSt	1	MLGSFGSSSSQSHPHHDEESSDDHHQ	RRFTAT	TTTTTT	TTSPAIQIRQLLISCAELI
LsAt	1	SDFSAAKRLLTILSTNSSPFGDSTERLVHQFTRALSRLNRYISSSTTNHFMTPVETTP			
LsLe	61	SDFSAAKRLLTILSTNSSPFGDSTERLVHQFTRALSRLNRYISSSTTNHFMTPVETTP			
LsSt	61	SDFSAAKRLLTILSTNSSPFGDSTERLVHQFTRALSRLNRYISSSTTNHFMTPVETTP			
LsAt	1	TDSSSLPSSSLALIQSSY	ELNQVTPFIRFTQLTANQAILEA	INGNHQAI	HIVDFDINH
LsLe	121	TDSSSLPSSSLALIQSSY	ELNQVTPFIRFTQLTANQAILEA	INGNHQAI	HIVDFDINH
LsSt	121	TDSSSLPSSSLALIQSSY	ELNQVTPFIRFTQLTANQAILEA	INGNHQAI	HIVDFDINH
LsAt	1	ERSSNPSSPP	LRITGGRD	TGLNRTGDRLL	ADSLGLQFQFHLLVIVEE
LsLe	178	ERSSNPSSPP	LRITGGRD	TGLNRTGDRLL	ADSLGLQFQFHLLVIVEE
LsSt	181	ERSSNPSSPP	LRITGGRD	TGLNRTGDRLL	ADSLGLQFQFHLLVIVEE
LsAt	54	LAGLLLOIR	LA	QGET	ANCVHLLH
LsLe	238	LAGLLLOIR	LA	QGET	ANCVHLLH
LsSt	241	LAGLLLOIR	LA	QGET	ANCVHLLH
LsAt	114	KEANH3DHS	FLRFB	EA	DDYMA
LsLe	297	KEANH3DHS	FLRFB	EA	DDYMA
LsSt	300	KEANH3DHS	FLRFB	EA	DDYMA
LsAt	174	ERK	RRHR	RF	EE
LsLe	357	ERK	RRHR	RF	EE
LsSt	360	ERK	RRHR	RF	EE
LsAt	230	DNQPLFSISSWR			
LsLe	417	DNQPLFSISSWR			
LsSt	420	DNQPLFSISSWR			

Fig. 8